Prevalence of Golden retriever in European dogs with lymphoma: preliminary data

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Abstract

Canine breeds, being genetic clusters, are good models for studies on genetic predisposition. Golden retriever (GR) has been described with a high incidence of both lymphoma overall (19%) and T zone lymphoma (TZL, 40%) with differences in different geographical areas in US. This breed predisposition is confirmed in Japanese but not in European (EU) case series although specific studies are still lacking (Modiano et al., 2005; Seelig et al., 2014).

Aim of the present study is to investigate the prevalence of GR in a huge case series of canine lymphomas from different EU countries and to compare prevalence of different subtypes with studies in extra-EU countries, in order to support a possible different genetic predisposition.

Signalment data on 1734 consecutive cases of canine lymphoma collected from 9 different European countries are retrospectively analysed. When subtypes are available, cases are furtherly separated in three subtype groups: 1) B-cell lymphoma, 2) T-cell lymphoma-high grade, 3) TZL. Odds ratio (OR) for different lymphoma subtypes are calculated in comparison with mixed breed population, considered as control.

Overall prevalence of GR is 5.19% (range 1.59-7.32%) of lymphoma cases and differs from that reported in American and Japanese caseloads. Prevalence slightly varies among EU countries and no subtypes predilection is found if compared with mixed breed. Concerning Italian cohort, GR is not predisposed to develop a lymphoma when normalized for the breed prevalence (OR=1.49, 95% confidence interval=0.87-2.55, p=0.14).

Prevalence of lymphoma in EU population of GR is much lower than that of US. No predisposition is identified in EU GR for TZL differently from US and Japan. Being genetic of European GR population quite different from American and Japanese ones this suggest a possible different genetic predisposition. Slight differences in GR lymphoma prevalence among European countries likely reflects different breed distribution rather than different genetic predisposition.

References
